

c 38	52.8	10.1	129149	46	HS510D11	298044	Human DNA s
c 39	52.8	10.1	137143	55	AC068496	AC068496	Mus muscu
c 40	52.6	10.0	175280	49	AC023327	AC023327	Homo sapi
c 41	52.6	10.0	177568	46	HS388M5	297055	Human DNA s
c 42	52.6	10.0	206051	50	AC024914	AC024914	Mus muscu
c 43	52.2	10.0	153147	46	HS13D10	AL021407	Homo sapi
c 44	52.2	10.0	155344	64	AL161899	AL161899	Homo sapi
c 45	52.2	10.0	170356	88	AF259072	AF259072	Mus muscu

#### ALIGNMENTS

**RESULT 1**  
**CVU20341**  
**LOCUS CVU20341 8158 bp DNA circular VRL 25-OCT-1995**  
**DEFINITION Cassava vein mosaic virus, complete genome.**  
**ACCESSION U20341**  
**VERSION U20341.1 GI:665931**  
**KEYWORDS .**  
**SOURCE Cassava vein mosaic virus.**  
**ORGANISM Cassava vein mosaic virus**  
**Viruses; Retroid viruses.**  
**REFERENCE 1 (bases 1 to 8158)**  
**AUTHORS Calvert,L.A., Ospina,M.D. and Shepherd,R.J.**  
**TITLE Characterization of cassava vein mosaic virus: a distinct plant pararetrovirus**  
**JOURNAL J. Gen. Virol. 76 (Pt 5), 1271-1278 (1995)**  
**MEDLINE 95248298**  
**REFERENCE 2 (bases 1 to 8158)**  
**AUTHORS Calvert,L.A.**  
**TITLE Direct Submission**  
**JOURNAL Submitted (26-JAN-1995) Lee A. Calvert, Virology Unit, Centro Internacional de Agricultura Tropical, A.A. 6713, Cali, Valle, Colombia**  
**FEATURES Location/Qualifiers**  
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 NLADRINYLQNINTSIDFKLWRMNKENLERQELLRQINELKEEIKSLKNIPSTVAI  
 PTNTYTINMIRTEDEWKYFKYIEKELVNQNKTEAIAKILDNSYIINDNLGLLYERYEE  
 INPTPKPYKRPEТИФDTPQYAKYIRNQRQEЕYEKQKELKNNENKEQFELEWKEKQ  
 QKDKGKGQITVYVPTLIIPDIKPEKQKHEDMMLEMIKLNQNELEQLKIQRHKEHEHQAE  
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90: gb_sts2:*
91: gb_sy:*
92: gb_un:*
93: gb_vil:*
94: gb_vl2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	514.6	98.2	8158	93	CVU20341		U20341 Cassava vei
2	514.6	98.2	8159	93	CVU59751		U59751 Cassava vei
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c 4	60.4	11.5	112585	46	HS1059E7		AL023095 Human DNA
5	59	11.3	276598	37	AC012382		AC012382 Mus muscu
6	58.4	11.1	193432	57	AC073290		AC073290 Mus muscu
7	58.2	11.1	259421	57	AC073689		AC073689 Mus muscu
c 8	58	11.1	171743	53	AC055806		AC055806 Homo sapi
9	57.6	11.0	204985	57	AC073938		AC073938 Mus muscu
c 10	57.6	11.0	237908	47	AC020971		AC020971 Mus muscu
11	57	10.9	163229	10	AC009039		AC009039 Homo sapi
12	56.8	10.8	211308	57	AC073613		AC073613 Homo sapi
13	56.2	10.7	513	88	RNU83985		U83985 Rattus norv
14	56.2	10.7	60058	48	AC022549		AC022549 Mus muscu
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16	56.2	10.7	159818	27	AC007337		AC007337 Homo sapi
17	56.2	10.7	204318	88	AC026387		AC026387 Mus muscu
c 18	55.6	10.6	115976	57	AC073502		AC073502 Homo sapi
c 19	55.6	10.6	153664	53	AC040971		AC040971 Homo sapi
c 20	55.2	10.5	136037	9	AC004104		AC004104 Homo sapi
c 21	55	10.5	161996	63	AL133401		AL133401 Mus muscu
22	55	10.5	181636	50	AC025108		AC025108 Homo sapi
23	55	10.5	194615	36	AC010184		AC010184 Homo sapi
c 24	55	10.5	200275	57	AC073883		AC073883 Mus muscu
25	54.6	10.4	71618	7	AB012240		AB012240 Arabidops
26	54.6	10.4	200573	49	AC024116		AC024116 Mus muscu
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28	54.2	10.3	147156	56	AC068998		AC068998 Mus muscu
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c 30	54	10.3	91748	88	AF177767		AF177767 Mus muscu
c 31	54	10.3	169328	35	AP000472		AP000472 Homo sapi
32	54	10.3	183330	38	AC015932		AC015932 Mus muscu
c 33	54	10.3	340000	35	AP001683		AP001683 Homo sapi
34	53.4	10.2	131169	84	AL356779		AL356779 Homo sapi
c 35	53.4	10.2	165313	84	AL356742		AL356742 Homo sapi
36	53	10.1	53899	8	F14010		AC026234 Sequence
37	53	10.1	221285	49	AC023611		AC023611 Mus muscu

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2000, 01:31:17 ; Search time 990.18 Seconds  
(without alignments)  
2311.309 Million cell updates/sec

Title: US-09-202-838-3  
Perfect score: 524

Sequence: 1 ggttaccagaaggtaattatc.....aaattttgaagtttgaattc 524

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_ba2:  
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4: gb\_ov:  
5: gb\_pat:  
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7: gb\_p11:  
8: gb\_p12:  
9: gb\_prl:  
10: gb\_pr2:  
11: gb\_pr3:  
12: em\_fun:  
13: em\_hum1:  
14: em\_hum2:  
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29: gb\_in1:\*

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